



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,895

DATE: 10/12/2004

TIME: 12:03:41

Input Set : A:\N12-038US Seg Listing.txt

Output Set: N:\CRF4\10122004\J729895.raw

(pg. 6)

**ENTERED**

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3 <110> APPLICANT: UNIVERSITY OF NEW MEXICO
5 <120> TITLE OF INVENTION: OUTCOME PREDICTION AND RISK CLASSIFICATION IN CHILDHOOD
6   LEUKEMIA
8 <130> FILE REFERENCE: N12-038US/310.00050101
10 <140> CURRENT APPLICATION NUMBER: 10/729,895
11 <141> CURRENT FILING DATE: 2003-12-05
13 <150> PRIOR APPLICATION NUMBER: 60/510,904
14 <151> PRIOR FILING DATE: 2003-10-14
16 <150> PRIOR APPLICATION NUMBER: 60/510,968
17 <151> PRIOR FILING DATE: 2003-10-14
19 <150> PRIOR APPLICATION NUMBER: 60/432,064
20 <151> PRIOR FILING DATE: 2002-12-06
22 <150> PRIOR APPLICATION NUMBER: 60/432,077
23 <151> PRIOR FILING DATE: 2002-12-06
25 <150> PRIOR APPLICATION NUMBER: 60/432,078
26 <151> PRIOR FILING DATE: 2002-12-06
28 <160> NUMBER OF SEQ ID NOS: 18
30 <170> SOFTWARE: PatentIn Ver. 3.2
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1080
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1026)
41 <400> SEQUENCE: 1
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43 Met Pro Phe Leu Leu Gly Leu Arg Gln Asp Lys Glu Ala Cys Val Gly
44   1             5             10             15
46 acc aac aat caa agc tac atc tgt gac aca gga cac tgc tgt gga cag      96
47 Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly His Cys Cys Gly Gln
48             20             25             30
50 tct cag tgc tgc aac tac tac tat gaa ctc tgg tgg ttc tgg ctg gtg     144
51 Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val
52             35             40             45
54 tgg acc atc atc atc atc ctg agc tgc tgc tgt gtt tgc cac cac cgc     192
55 Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys Val Cys His His Arg
56             50             55             60
58 cga gcc aag cac cgc ctt cag gcc cag cag cgg caa cat gaa atc aac     240
59 Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg Gln His Glu Ile Asn
60 65             70             75             80
62 ctg atc gct tac cga gaa gcc cac aat tac tca gcg ctg cca ttt tat     288
63 Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser Ala Leu Pro Phe Tyr

```

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64		85		90		95	
66	ttc agg ttt ttg cca aac tat tta cta cct cct tat gag gaa gtg gtg						336
67	Phe Arg Phe Leu Pro Asn Tyr Leu Leu Pro Pro Tyr Glu Glu Val Val						
68		100		105		110	
70	aac cga cct cca act cct ccc cca cca tac agt gcc ttc cag cta cag						384
71	Asn Arg Pro Pro Thr Pro Pro Pro Tyr Ser Ala Phe Gln Leu Gln						
72		115		120		125	
74	cag cag cag ctg ctg cct cca cag tgt ggc cct gca ggt ggc agt ccc						432
75	Gln Gln Gln Leu Leu Pro Pro Gln Cys Gly Pro Ala Gly Gly Ser Pro						
76		130		135		140	
78	ccg ggc atc gat ccc acc agg gga tcc cag ggg gca cag agc agc ccc						480
79	Pro Gly Ile Asp Pro Thr Arg Gly Ser Gln Gly Ala Gln Ser Ser Pro						
80	145		150		155		160
82	ttg tct gag ccc agc aga agc agc aca aga ccc cca agc atc gct gac						528
83	Leu Ser Glu Pro Ser Arg Ser Ser Thr Arg Pro Pro Ser Ile Ala Asp						
84		165		170		175	
86	cct gat ccc tct gac cta cca gtt gac cga gca gcc acc aaa gcc cca						576
87	Pro Asp Pro Ser Asp Leu Pro Val Asp Arg Ala Ala Thr Lys Ala Pro						
88		180		185		190	
90	ggg atg gag ccc agt ggc tct gtg gct ggc ctg ggg gag ctg gac ccg						624
91	Gly Met Glu Pro Ser Gly Ser Val Ala Gly Leu Gly Glu Leu Asp Pro						
92		195		200		205	
94	ggg gcc ttc ctg gac aaa gat gca gaa tgt agg gag gag ctg ctg aaa						672
95	Gly Ala Phe Leu Asp Lys Asp Ala Glu Cys Arg Glu Glu Leu Leu Lys						
96		210		215		220	
98	gat gac agc tct gaa cac ggc gca ccc gac agc aaa gag aag acg cct						720
99	Asp Asp Ser Ser Glu His Gly Ala Pro Asp Ser Lys Glu Lys Thr Pro						
100	225		230		235		240
102	ggg aga cat cgc cgc ttc aca ggt gac tgc ggc att gaa gtg tgt gtg						768
103	Gly Arg His Arg Arg Phe Thr Gly Asp Ser Gly Ile Glu Val Cys Val						
104		245		250		255	
106	tgc aac cgg ggc cac cat gac gat gac ctc aaa gag ttc aac aca ctc						816
107	Cys Asn Arg Gly His His Asp Asp Asp Leu Lys Glu Phe Asn Thr Leu						
108		260		265		270	
110	atc gat gat gct ctg gat ggg ccc ctg gac ttc tgc gac agc tgc cat						864
111	Ile Asp Asp Ala Leu Asp Gly Pro Leu Asp Phe Cys Asp Ser Cys His						
112		275		280		285	
114	gtg cgg ccc cct ggt gat gag gag gaa ggc ctc tgt cag tcc tct gag						912
115	Val Arg Pro Pro Gly Asp Glu Glu Glu Gly Leu Cys Gln Ser Ser Glu						
116		290		295		300	
118	gag cag gct cga gag cct ggg cac ccg cac ctg cca cgg ccg ccc gca						960
119	Glu Gln Ala Arg Glu Pro Gly His Pro His Leu Pro Arg Pro Pro Ala						
120	305		310		315		320
122	tgc ctg ctg ctg aac acc atc aac gag cag gac tct ccc aac tcc cag						1008
123	Cys Leu Leu Leu Asn Thr Ile Asn Glu Gln Asp Ser Pro Asn Ser Gln						
124		325		330		335	
126	agc agc agc tcc ccc agc tagagcaggt cctgccagca cccagcaact						1056
127	Ser Ser Ser Ser Pro Ser						
128		340					

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130 tggcaaagca accagggtag ggga                                     1080
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 342
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 2
139 Met Pro Phe Leu Leu Gly Leu Arg Gln Asp Lys Glu Ala Cys Val Gly
140   1           5           10           15
142 Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly His Cys Cys Gly Gln
143           20           25           30
145 Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val
146           35           40           45
148 Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys Val Cys His His Arg
149           50           55           60
151 Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg Gln His Glu Ile Asn
152   65           70           75           80
154 Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser Ala Leu Pro Phe Tyr
155           85           90           95
157 Phe Arg Phe Leu Pro Asn Tyr Leu Leu Pro Pro Tyr Glu Glu Val Val
158           100          105          110
160 Asn Arg Pro Pro Thr Pro Pro Pro Tyr Ser Ala Phe Gln Leu Gln
161           115          120          125
163 Gln Gln Gln Leu Leu Pro Pro Gln Cys Gly Pro Ala Gly Gly Ser Pro
164           130          135          140
166 Pro Gly Ile Asp Pro Thr Arg Gly Ser Gln Gly Ala Gln Ser Ser Pro
167 145           150          155          160
169 Leu Ser Glu Pro Ser Arg Ser Ser Thr Arg Pro Pro Ser Ile Ala Asp
170           165          170          175
172 Pro Asp Pro Ser Asp Leu Pro Val Asp Arg Ala Ala Thr Lys Ala Pro
173           180          185          190
175 Gly Met Glu Pro Ser Gly Ser Val Ala Gly Leu Gly Glu Leu Asp Pro
176           195          200          205
178 Gly Ala Phe Leu Asp Lys Asp Ala Glu Cys Arg Glu Glu Leu Leu Lys
179           210          215          220
181 Asp Asp Ser Ser Glu His Gly Ala Pro Asp Ser Lys Glu Lys Thr Pro
182 225           230          235          240
184 Gly Arg His Arg Arg Phe Thr Gly Asp Ser Gly Ile Glu Val Cys Val
185           245          250          255
187 Cys Asn Arg Gly His His Asp Asp Asp Leu Lys Glu Phe Asn Thr Leu
188           260          265          270
190 Ile Asp Asp Ala Leu Asp Gly Pro Leu Asp Phe Cys Asp Ser Cys His
191           275          280          285
193 Val Arg Pro Pro Gly Asp Glu Glu Glu Gly Leu Cys Gln Ser Ser Glu
194           290          295          300
196 Glu Gln Ala Arg Glu Pro Gly His Pro His Leu Pro Arg Pro Pro Ala
197 305           310          315          320
199 Cys Leu Leu Leu Asn Thr Ile Asn Glu Gln Asp Ser Pro Asn Ser Gln
200           325          330          335
202 Ser Ser Ser Ser Pro Ser

```

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```

203          340
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1140
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <220> FEATURE:
213 <221> NAME/KEY: CDS
214 <222> LOCATION: (1)..(1089)
216 <400> SEQUENCE: 3
217 atg gag agg aga agg ctc ctg ggt ggc atg gcg ctc ctg ctc ctc cag 48
218 Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
219 1 5 10 15
221 gcg ctg ccc agc ccc ttg tca gcc agg gct gaa ccc ccg cag gat aag 96
222 Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
223 20 25 30
225 gaa gcc tgt gtg ggt acc aac aat caa agc tac atc tgt gac aca gga 144
226 Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
227 35 40 45
229 cac tgc tgt gga cag tct cag tgc tgc aac tac tac tat gaa ctc tgg 192
230 His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
231 50 55 60
233 tgg ttc tgg ctg gtg tgg acc atc atc atc atc ctg agc tgc tgc tgt 240
234 Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
235 65 70 75 80
237 gtt tgc cac cac cgc cga gcc aag cac cgc ctt cag gcc cag cag cgg 288
238 Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
239 85 90 95
241 caa cat gaa atc aac ctg atc gct tac cga gaa gcc cac aat tac tca 336
242 Gln His Glu Ile Asn Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser
243 100 105 110
245 gcg ctg cca ttt tat ttc agg ttt ttg cca aac tat tta cta cct cct 384
246 Ala Leu Pro Phe Tyr Phe Arg Phe Leu Pro Asn Tyr Leu Leu Pro Pro
247 115 120 125
249 tat gag gaa gtg gtg aac cga cct cca act cct ccc cca cca tac agt 432
250 Tyr Glu Glu Val Val Asn Arg Pro Pro Thr Pro Pro Pro Pro Tyr Ser
251 130 135 140
253 gcc ttc cag cta cag cag cag cag ctg ctg cct cca cag tgt ggc cct 480
254 Ala Phe Gln Leu Gln Gln Gln Leu Leu Pro Pro Gln Cys Gly Pro
255 145 150 155 160
257 gca ggt ggc agt ccc ccg ggc atc gat ccc acc agg gga tcc cag ggg 528
258 Ala Gly Gly Ser Pro Pro Gly Ile Asp Pro Thr Arg Gly Ser Gln Gly
259 165 170 175
261 gca cag agc agc ccc ttg tct gag ccc agc aga agc agc aca aga ccc 576
262 Ala Gln Ser Ser Pro Leu Ser Glu Pro Ser Arg Ser Ser Thr Arg Pro
263 180 185 190
265 cca agc atc gct gac cct gat ccc tct gac cta cca gtt gac cga gca 624
266 Pro Ser Ile Ala Asp Pro Asp Pro Ser Asp Leu Pro Val Asp Arg Ala
267 195 200 205
269 gcc acc aaa gcc cca ggg atg gag ccc agt ggc tct gtg gct ggc ctg 672

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```

270 Ala Thr Lys Ala Pro Gly Met Glu Pro Ser Gly Ser Val Ala Gly Leu
271      210                      215                      220
273 ggg gag ctg gac ccg ggg gcc ttc ctg gac aaa gat gca gaa tgt agg      720
274 Gly Glu Leu Asp Pro Gly Ala Phe Leu Asp Lys Asp Ala Glu Cys Arg
275 225                      230                      235                      240
277 gag gag ctg ctg aaa gat gac agc tct gaa cac ggc gca ccc gac agc      768
278 Glu Glu Leu Leu Lys Asp Asp Ser Ser Glu His Gly Ala Pro Asp Ser
279      245                      250                      255
281 aaa gag aag acg cct ggg aga cat cgc cgc ttc aca ggt gac tcg ggc      816
282 Lys Glu Lys Thr Pro Gly Arg His Arg Arg Phe Thr Gly Asp Ser Gly
283      260                      265                      270
285 att gaa gtg tgt gtg tgc aac cgg ggc cac cat gac gat gac ctc aaa      864
286 Ile Glu Val Cys Val Cys Asn Arg Gly His His Asp Asp Asp Leu Lys
287      275                      280                      285
289 gag ttc aac aca ctc atc gat gat gct ctg gat ggg ccc ctg gac ttc      912
290 Glu Phe Asn Thr Leu Ile Asp Asp Ala Leu Asp Gly Pro Leu Asp Phe
291      290                      295                      300
293 tgc gac agc tgc cat gtg cgg ccc cct ggt gat gag gag gaa ggc ctc      960
294 Cys Asp Ser Cys His Val Arg Pro Pro Gly Asp Glu Glu Glu Gly Leu
295 305                      310                      315                      320
297 tgt cag tcc tct gag gag cag gct cga gag cct ggg cac ccg cac ctg      1008
298 Cys Gln Ser Ser Glu Glu Gln Ala Arg Glu Pro Gly His Pro His Leu
299      325                      330                      335
301 cca cgg ccg ccc gca tgc ctg ctg ctg aac acc atc aac gag cag gac      1056
302 Pro Arg Pro Pro Ala Cys Leu Leu Leu Asn Thr Ile Asn Glu Gln Asp
303      340                      345                      350
305 tct ccc aac tcc cag agc agc agc tcc ccc agc tagagcaggt cctgccagca 1109
306 Ser Pro Asn Ser Gln Ser Ser Ser Ser Pro Ser
307      355                      360
309 cccagcaact tggcaaagca accagggtag g      1140
312 <210> SEQ ID NO: 4
313 <211> LENGTH: 363
314 <212> TYPE: PRT
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 4
318 Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
319 1      5      10      15
321 Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
322      20      25      30
324 Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
325      35      40      45
327 His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
328      50      55      60
330 Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
331 65      70      75      80
333 Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
334      85      90      95
336 Gln His Glu Ile Asn Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser
337      100      105      110

```

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 4

**VERIFICATION SUMMARY**

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Input Set : A:\N12-038US Seg Listing.txt

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L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0